In the Specification

Please amend the specification as shown:

In order to clarify applicants' previous amendment to the specification, applicants request the following:

Please delete the paragraph on page 28, lines 15-30, which reads:

> Polypeptides in the EGF family appear, in some ways, unrelated. For example, TGF-α and EGF have only 30% structural homology (Marquardt et al., Science 223:1079-1082, 1984). However, they display similar binding kinetics for, and stimulate tyrosine-specific phosphorylation of, the Mr 180,000 EGF membrane receptor (Cohen et al., J Biol. Chem. 255:4834-4842, 1980; Reynolds et al., Nature 292:259-262, 1981). The functional equivalence of the two growth factors is partly attributed to the same relative positioning of six cysteine residues, represented by "C" in the consensus sequence: $CX_7CX_{4,5}CX_{10}CXCX_8C$. These conserved residues impose similar disulfide bond-mediated structural constraints and, thus, a related three-dimensional structure (Twardzik et al., Proc. Natl. Acad. Sci. USA 82:5300-5304, 1985). Those of ordinary skill in the art are well able to compare any given amino acid sequence with the EGF-family consensus sequence to determine whether a polypeptide is likely to be functionally equivalent to EGF (and, if so, useful in practicing the methods of the present invention); (see, e.g., Blomquist et al., Proc. Natl. Acad. Sci. USA 81:7363-7367, 1984, for a description of a computer search that revealed a similar pattern of cysteine and glycine residues in EGF, TGF-α, and the sequence of a 19 kDa early protein of vaccinia virus).

Replace the paragraph with the following paragraph:

Polypeptides in the EGF family appear, in some ways, unrelated. For example, TGF-α and EGF have only 30% structural homology (Marquardt et al., Science 223:1079-1082, 1984). However, they display similar binding kinetics for, and stimulate tyrosine-specific phosphorylation of, the Mr 180,000 EGF membrane receptor (Cohen et al., J Biol. Chem. 255:4834-4842, 1980; Reynolds et al., Nature 292:259-262, 1981). The functional equivalence of the two growth factors is partly attributed to the same relative positioning of six cysteine

residues, represented by "C" in the consensus sequence: $CX_7CX_{4,5}CX_{10}CXCX_8C$ (SEQ ID NO: 1). These conserved residues impose similar disulfide bond-mediated structural constraints and, thus, a related three-dimensional structure (Twardzik et al., Proc. Natl. Acad. Sci. USA 82:5300-5304, 1985). Those of ordinary skill in the art are well able to compare any given amino acid sequence with the EGF-family consensus sequence to determine whether a polypeptide is likely to be functionally equivalent to EGF (and, if so, useful in practicing the methods of the present invention); (see, e.g., Blomquist et al., Proc. Natl. Acad. Sci. USA 81:7363-7367, 1984, for a description of a computer search that revealed a similar pattern of cysteine and glycine residues in EGF, TGF-α, and the sequence of a 19 kDa early protein of vaccinia virus).